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| #31 | Search site specific recombination, gram positive | 13:58:04 | <u>45</u> |
| #30 | Search site-specificrecombination, gram positive | 13:50:07 | <u> 1629</u> |
| <u>#24</u> | Search intramolecular recombination, gram positive | 13:49:51 | <u>4</u> |
| <u>#11</u> | Search beta recombinase | 13:49:35 | <u>958</u> |
| <u>#29</u> | Search b | 13:49:26 | <u>684797</u> |
| <u>#23</u> | Search intramolecular recombination activity, gram | 13:25:07 | . 0 |
| | positive | | |
| #22 | Search intramolecular recombination activity, beta | 13:24:49 | · <u>2</u> |
| | recombinase | | |
| <u>#21</u> | Search intramolecular recombination activity | 13:24:42 | <u>216</u> |
| <u>#12</u> | Search beta recombinase, review | 12:58:46 | <u>38</u> . |
| <u>#10</u> | Search Gene Therapy Inc | 12:17:31 | <u>613</u> |
| . <u>#8</u> | Search Lechardeur | 12:13:50 | <u>21</u> |
| <u>#7</u> | Search galactosyl spermine | 09:33:02 | <u>1</u> |
| <u>#6</u> | Search glactosyl spermine | 09:32:57 | <u>0</u> |
| <u>#5</u> | Search mannosyl spermine | 09:32:51 | <u>0</u> |
| <u>#4</u> | Search lactosyl spermine | 09:32:45 | <u>0</u> |
| #2 | Search cholesteryl spermine | 09:31:03 | <u>7</u> |
| <u>#1</u> | Search cholesteryl spermine, lactosyl spermine | 09:30:49 | <u>0</u> |

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Nov 6 2006 15:24:20

Application/Control Number: 10/808,161

Art Unit: 1633



Appendix

Site-specific recombinase [Streptococcus pyogenes], plasmid pSM19035 Accession YP 232767.1 GI:63021996

 $\label{lem:makigyarvsskeqnldrqlqalqgvskvfsdklsgqsverpqlqamlnyiregdivvvteldrlgrnnkeltelmnaiqqkgatlevlnlpsmngiedenlrrlinnlvielykyqaeserkrikerqaqgieiakskgkfkgrqhkfkendprlkhafdlflngcsdkeveeqtginrrtfrryrtrynvtvdqrknkgkrds$

| | Score | E |
|---|--------|-------|
| A partial list of sequences producing significant alignments | (Bits) | Value |
| | | |
| gi 63021985 ref YP_232754.1 site-specific recombinase [Strep | 316 | 3e-85 |
| gi 81176607 gb ABB59535.1 putative resolvase [Pediococcus acidi | 305 | 7e-82 |
| gi 10956207 ref NP_044464.1 resolvase [Streptococcus agalact | 302 | 8e-81 |
| gi 392559 gb AAA73395.1 resolvase protein [Streptococcus agalac | 301 | 1e-80 |
| gi 6690329 gb AAF24086.1 AF117258_3 resolvase [Staphylococcus au | 297 | 2e-79 |
| gi 3023049 gb AAC38605.1 resolvase [Enterococcus faecalis] | 293 | 4e-78 |
| gi 6746431 gb AAF27558.1 putative resolvase [Lactococcus lactis | 254 | 1e-66 |
| gi 6739586 gb AAF27319.1 putative resolvase [Lactococcus lactis | 251 | 1e-65 |
| gi 58701072 gb AAW81284.1 hypothetical protein [Lactobacillus p | 236 | 3e-61 |
| gi 108736165 gb ABG00294.1 ORF12 [Lactococcus lactis] | 236 | 4e-61 |
| gi 116334884 ref YP_796409.1 Site-specific recombinase, DNA | 235 | 1e-60 |
| gi 56707177 ref YP_163807.1 putative resolvase [Lactobacillu | 234 | 2e-60 |
| gi 75181775 gb ABA12807.1 hypothetical protein [Lactobacillus p | 233 | 3e-60 |
| gi 75182232 gb ABA12841.1 conserved hypothetical protein [La | 233 | 4e-60 |
| gi 5420101 emb CAB46556.1 putative resolvase [Streptococcus the | 231 | 2e-59 |
| gi 29377950 ref NP_817076.1 site-specific recombinase, resol | 216 | 5e-55 |
| gi 69247432 ref ZP_00604345.1 recombinase Sin [Enterococcus | 185 | 1e-45 |
| gi 116326678 ref YP_796452.1 Site-specific recombinase, DNA | 156 | 6e-37 |
| gi 116490744 ref YP_810288.1 Site-specific recombinase, DNA | 134 | 2e-30 |
| gi 69247633 ref ZP_00604427.1 Resolvase, N-terminal: Resolvas | 133 | 4e-30 |
| gi 69250457 ref ZP_00605155.1 Resolvase, N-terminal [Enteroc | 129 | 8e-29 |
| gi 81330302 ref YP_398694.1 hypothetical protein pHTbeta_52 | 127 | 4e-28 |
| gi 116493435 ref YP_805170.1 Site-specific recombinase, DNA | 119 | 7e-26 |
| gi 37595767 ref NP_932185.1 Res2 [Staphylococcus aureus] >gi | 117 | 2e-25 |
| gi 82743151 ref ZP_00905814.1 integrative genetic element Gs | 115 | 1e-24 |
| gi 495089 gb AAA26675.1 recombinase >gi 8574415 emb CAB94806 | 115 | 2e-24 |
| gi 1086524 gb AAB08926.1 invertase-enterococcal | 113 | 4e-24 |
| gi 82751033 ref YP_416774.1 recombinase [Staphylococcus aure | 112 | 1e-23 |
| gi 22476843 gb AAM97333.1 AF426833_2 recombinase Sin [Staphyloco | 111 | 2e-23 |
| gi 13793990 gb AAK38455.1 recombinase Sin [Staphylococcus epide | 110 | 3e-23 |
| gi 22476850 gb AAM97339.1 AF426834_5 recombinase Sin [Staphyloco | 110 | 5e-23 |
| gi 70727309 ref YP_254225.1 recombinase Sin [Staphylococcus | 109 | 6e-23 |
| gi 11230707 emb CAC16669.1 recombinase [Staphylococcus haemolyt | 109 | 9e-23 |
| gi 8980455 emb CAB96927.1 Bin3 protein [Stenotrophomonas maltop | 108 | 2e-22 |
| gi 38257108 ref NP_940770.1 recombinase [Staphylococcus warn | 107 | 3e-22 |
| gi 116514884 ref YP_813790.1 Site-specific recombinase, DNA | 107 | 5e-22 |
| gi 111017138 ref YP_700110.1 possible resolvase, N-terminal | 106 | 6e-22 |
| gi 11968214 ref NP_072000.1 recombinase [Enterococcus faecal | 105 | 1e-21 |
| gi 110628945 gb ABG79938.1 resolvase [Lactobacillus reuteri] | 104 | 2e-21 |
| gi 32455946 ref NP_862404.1 putative transposon resolvase [M | 104 | 3e-21 |
| \cdot | | |

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Example Alignment

gi|116326678|ref|YP_796452.1| Site-specific recombinase, DNA invertase Pin related protein, [Lactobacillus casei ATCC 334] gi|116106496|gb|ABJ71637.1| Site-specific recombinase, DNA invertase Pin related protein, [Lactobacillus casei ATCC 334]

Score = 156 bits (394), Expect = 6e-37, Method: Composition-based stats.
Identities = 88/156 (56%), Positives = 121/156 (77%), Gaps = 2/156 (1%)

| Query | 1 | MAKIGYARVSSKEQNLDRQLQALQGVSKVFSDKLSGQSVERPQLQAMLNYIREGDIVV M+KIGYARVS+++QNL RQ++ L GV+K+F +KLSG++ +RPQL+AML+YIR+ D VV | 58 |
|-------|-----|--|-----|
| Sbjct | 1 | MSKIGYARVSTRDQNLARQIEQLHDAGVNKIFQEKLSGKNADRPQLKAMLDYIRDDDEVV | 60 |
| Query | 59 | VTELDRLGRNNKELTELMNAIQQKGATLEVLNLPSMNGIEDENLRRLINNLVIELYKYQA V LDRLGRN+ +LT+++ I+ +GA L VLNLPS IED NLR LI +++ELYKY A | 118 |
| Sbjct | 61 | VLSLDRLGRNSHDLTDIIETIRHRGAQLNVLNLPSFASIEDPNLRNLITTIIVELYKYIA | 120 |
| Query | 119 | ESERKRIKERQAQGIEIAKSKGKFKGRQHKFKENDP 154 + ER+ IK RQ QGIEIAK +GK+KG+ ++ + P | |

Sbjct 121 QEERETIKIRQQQGIEIAKRQGKYKGKIREYGPHSP 156